

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> Novel genes of Candida albicans and the proteins
coded by these genes.

<130> 2517 PCT SEQUENCES IN FRENCH

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<150> FR 9907250

<151> 1999-06-09

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 747

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(747)

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<222> (136)..(138)

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cta act ata aat gat gta tca aaa tca gga ttt gga tac aat ccg tcc	96
Leu Thr Ile Asn Asp Val Ser Lys Ser Gly Phe Gly Tyr Asn Pro Ser	
20 25 30	
ata gga cca ata tca aat act att acc cta gaa tct tca ctg gta tta	144
Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu	
35 40 45	
tta aat aaa cgt aca ata tca tta aca cca aca tca tct gac tcc att	192
Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile	
50 55 60	
tat gat aga aat att atc acg aaa aag cca cac gaa atc aac tta tct	240
Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser	
65 70 75 80	
tcg tta tca ttt ttg ttt tgt gag att att agt tgg gca cac tct aat	288
Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn	
85 90 95	
tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat	336
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr	
100 105 110	
caa ata ggt caa cga tat ctc gaa ttg tgt aaa ata aga gaa ggt ttt	384
Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe	
115 120 125	
aaa aac agt aaa cga gag att aga ctt ttg gaa atg tta caa ttt att	432
Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile	
130 135 140	
cat ggt ccg ttc tgg aaa ttg att ttt ggt aaa act gct aat gaa tta	480
His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu	
145 150 155 160	

gaa aaa tcg caa gat ttg ccc aat gaa tat atg att gtg gag aat gtg 528
 Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
 165 170 175

cca tta tta aat aga ttt att agt ata cct aag gag tat ggc gac tta 576
 Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
 180 185 190

aat tgt tca gca ttt gtt gcg ggt ata att gag gga gca ctt gat aat 624
 Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
 195 200 205

agt gga ttc aat gcc gat gtt aca gca cac acg gtc gct aca gat gca 672
 Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
 210 215 220

aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta 720
 Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu
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att aga gag agt ttg aga ttt gga taa 747
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<213> Candida albicans

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Ile Gly Pro Ile Ser Asn Thr Ile Thr Leu Glu Ser Ser Ser Val Leu
 35 40 45

Leu Asn Lys Arg Thr Ile Ser Leu Thr Pro Thr Ser Ser Asp Ser Ile
 50 55 60

Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
 65 70 75 80

Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
 85 90 95

Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
 100 105 110

Gln Ile Gly Gln Arg Tyr Leu Glu Leu Cys Lys Ile Arg Glu Gly Phe
 115 120 125

Lys Asn Ser Lys Arg Glu Ile Arg Leu Leu Glu Met Leu Gln Phe Ile
 130 135 140

His Gly Pro Phe Trp Lys Leu Ile Phe Gly Lys Thr Ala Asn Glu Leu
 145 150 155 160

Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
 165 170 175

Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu
 180 185 190

Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn
 195 200 205

Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala
 210 215 220

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Ile Arg Glu Ser Leu Arg Phe Gly

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gaa aag att agc agt aaa aca tcg tct atc aac tta tat caa gac ttg 96

Glu Lys Ile Ser Ser Lys Thr Ser Ser Ile Asn Leu Tyr Gln Asp Leu

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cta aqa gct atg atc aac qaa cgt atg gct ccg qaa tta ttg cca tac 144

Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr

35 40 45

aaa caa gat tta atg tcc act gtt tta aca atg atg tct aac caa caa 192

Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln

50 55 60

caa tat tta tta gaa tct cac gaa tat ggt gat atg aat ggc gac agt 240

Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser

65 70 75 80

ggc gta tta tcc gga gac ttt aaa tta caa cta atg att atc gaa act 238
 Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr

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gat tta gag cgt ctc aac tat att gtt cga tta tac ata cga act cga 336
 Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg

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ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt 384
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caa aat gat aat tta ttg tcc aaa gag gaa aga gat tat ata cac aaa 432
 Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys

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tat ttc cag att ttg act caa tta tat aac aac tgt ttc ctc aaa aaa 480
 Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys

145

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155

160

cta cca caa atg ttg acc tat ttg gat gac acc agt ggt gga caa tca 528
 Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser

165

170

175

atg atc gtt gag cca gat tta gac cag cct gtg ttt atc aaa tgt acc 576
 Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr

180

185

190

ctg gaa gtc cca ata tta cta gat tac gac ggt gct aca gag ata gat 624
 Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp

195

200

205

tta gaa tta ata aaa aag gga gtc tac gtg gtg aaa tac agc cta gtc 672
 Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val

210

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25

30

Leu Arg Ala Met Ile Asn Glu Arg Met Ala Pro Glu Leu Leu Pro Tyr

35

40

45

Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln

50

55

60

Gln Tyr Leu Leu Glu Ser His Glu Tyr Gly Asp Met Asn Gly Asp Ser

65

70

75

80

Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr

85

90

95

Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg

100

105

110

Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser

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125

Gln Asn Asp Asn Leu Leu Ser Lys Glu Glu Arg Asp Tyr Ile His Lys

130

135

140

Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys
 145 150 155 160

Leu Pro Gln Met Leu Thr Tyr Leu Asp Asp Thr Ser Gly Gly Gln Ser
 165 170 175

Met Ile Val Glu Pro Asp Leu Asp Gln Pro Val Phe Ile Lys Cys Thr
 180 185 190

Ser Glu Val Pro Ile Leu Leu Asp Tyr Asp Gly Ala Thr Glu Ile Asp
 195 200 205

Leu Glu Leu Ile Lys Lys Gly Val Tyr Val Val Lys Tyr Ser Leu Val
 210 215 220

Lys Arg Tyr Ile Asp Ile Gly Asp Val Val Leu Ile
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Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys

20 25 30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gaa 144
 Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
 35 40 45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192
 Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240
 Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

gag att ttg caa gag cgt gag gag tta cta aag ggt tta gat cct aaa 288
 Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
 85 90 95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac 336
 Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
 100 105 110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga 384
 His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
 115 120 125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa 432
 Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
 130 135 140

tta gat aag gaa gat gtg gac cgt gca ttg ggt ata agt tca tta tcc 480
 Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
 145 150 155 160

tta tct gaa cct gag ggt ggc agt aat acg aaa aaa gtc gct ttc gac 528
 Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
 165 170 175

gat aat atc aag acg gtt aaa ttt gaa gat ttg gat gat gga att gaa 576
 Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
 180 185 190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt 624
 Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
 195 200 205

cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat 672
 Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
 210 215 220

agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa 720
 Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
 225 230 235 240

cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat 768
 Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
 245 250 255

gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg 816
 Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
 260 265 270

atg aca cag cca atg cca aaa caa ttg tct acc gtt tat gaa tca ata 864
 Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
 275 280 285

tct gat atg aga ttt gac ttt aaa gga gat tta att gaa ttg ggt cca 912
 Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
 290 295 300

gag gga gaa gaa cca aaa gat agt tca tcc gaa ata cct act tat atg 960
 Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
 305 310 315 320

gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg 1008
 Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
 325 330 335

ggt gag ttg gca cat tta gcc aga tcg act tta gct gga caa aga tgc 1056
 Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

ttg agc att caa aca tta ggg aga atc tta cat aaa ttg gga tta cat 1104
 Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152
 Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1248
 Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296
 Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344
 Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383
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 450 455 460

<211> 461

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<213> Candida albicans

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Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
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Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
 35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
 85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
 100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
 115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
 130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
 145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
 165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Asp Leu Asp Asp Gly Ile Glu
 180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
 195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
 210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
 225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
 245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
 260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
 275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Gly Pro
 290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Ser Glu Ile Pro Thr Tyr Met
 305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
 325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
 405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
 435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
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<210> 7

<211> 1383

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<222> (1)..(1380)

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gaa cca acc cca aaa ccc aca att ggt gga ttc ccc gaa ctt aaa aaa 96
 Glu Pro Thr Pro Lys Pro Thr Ile Gly Gly Phe Pro Glu Leu Lys Lys
 20 25 30

tta aaa gaa aag aaa gtc tca aga tgg agg caa aag caa caa cag gag 144
 Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Gln Glu
 35 40 45

cag agc aca act tcc cca aaa act act gaa atc cgt tca gag gct tcc 192
Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser

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55

60

aaa att cac caa gaa aat atc gag aag atg gct caa atg tca gag gaa 240
Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu

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gag att ttg caa gag cgt gag gag tta cta aag ggt tta gac cct aaa 288
Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys

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90

95

tta att gaa agt ttg att ggt aga tcc aag aaa agg gaa gca aca gac 336
Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp

100

105

110

cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga 384
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly

115

120

125

tgg att gga tca atg aaa act tct gaa gga tta aca gat tta tct caa 432
Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln

130

135

140

tta gat aag gaa gat gtg gac cgt gct ttg ggt ata agt tca tta tcc 480
Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser

145

150

155

160

tta tct gaa cct gag ggt ggc agc aat acg aaa aaa gtc gct ttc gac 528
Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp

165

170

175

gat aat atc aag acg gtt aaa ttt gaa gct ttg gat gat gaa att gaa 576
Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu

180

185

190

ttg gat cca aat gga tgg gag gac gtt act gat gtc aat gaa tta gtt	624
Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val	
195 200 205	
cct aat aat gat cac att gca cct gac gat tac cag att aat cct gat	672
Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp	
210 215 220	
agc gat gaa gaa gga ttg aat aat act gtt cat ttt aca aaa ccc aaa	720
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys	
225 230 235 240	
cag cca gat ttg gat ata aat gat ccc gat ttc ttt gat aag cta cat	768
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His	
245 250 255	
gag aaa tac tat cct gat ttg cct aaa gaa aca gaa aag ttg tca tgg	816
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp	
260 265 270	
atg aca cag cca atg cca aaa caa ttg tct aca gtt tat gaa tca ata	864
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile	
275 280 285	
tct gat atg aga ttt gac ttc aaa gga gat tta att gaa ttg agc gca	912
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala	
290 295 300	
gag gga gaa gaa cca aaa gat agt tca ttc gaa ata cct act tat atg	960
Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met	
305 310 315 320	
gga ctt cat cat cat tcg gag aac cca cat atg gca ggt tat aca ttg	1008
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu	
325 330 335	

ggt gag ttg gca cat tta gcc aga tgg act tta gct gga caa aga tgc 1056
 Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

ttg agc att caa aca tta ggg aga ata tta cat aaa ttg gga tta cat 1104
 Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca 1152
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 370 375 380

gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac 1200
 Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat 1248
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 405 410 415

gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca 1296
 Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
 420 425 430

ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa 1344
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 435 440 445

acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa 1383
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 450 455 460

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<213> Candida albicans

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Leu Lys Glu Lys Lys Val Ser Arg Trp Arg Gln Lys Gln Gln Glu
 35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
 50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
 65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
 85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
 100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
 115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
 130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
 145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
 165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
 180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
 195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp
 210 215 220

Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys
 225 230 235 240

Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His
 245 250 255

Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp
 260 265 270

Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile
 275 280 285

Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala
 290 295 300

Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met
 305 310 315 320

Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu
 325 330 335

Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys
 340 345 350

Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His
 355 360 365

Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr
 370 375 380

Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp
 385 390 395 400

20

Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp
405 410 415

Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala
420 425 430

Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln
435 440 445

Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys
450 455 460

<210> 9

<211> 2262

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(2262)

<220>

<221> modified_base

<222> (1093)..(1095)

<220>

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<222> (1828)..(1830)

<400> 9

atg gca gca gca cca cca cca cca gcg aaa aac cag ggt aag gca aaa 48
Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys
1 5 10 15

cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag 96
Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa 576
 Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
 180 185 190

ttg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca 624
 Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
 195 200 205

cga aac ccg ttt ttg tct atg gac ccc agc aac att cta tcg tac gag 672
 Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
 210 215 220

gag ttg tcg tcg tac att gtg gat cag ttt aaa agt gca gtg aaa aca 720
 Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
 225 230 235 240

agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat ata tcg 768
 Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
 245 250 255

acg aca gct tta aaa gag aga ttg tcg aag gaa ata aag tat gaa ccg 816
 Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
 260 265 270

ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtg aga 864
 Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
 275 280 285

cct att ccc aaa ttg ttt gag ttg ttc ggc aga cct gtt tat gat cat 912
 Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
 290 295 300

tgg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca 960
 Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
 305 310 315 320

ctc aaa ttt gag gat cct aac tgg aac gaa aag gaa aac gac aat gac 1008
 Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
 325 330 335

cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg 1056
 Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
 340 345 350

aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag 1104
 Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys
 355 360 365

tgg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag 1152
 Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
 370 375 380

atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc 1200
 Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
 385 390 395 400

agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac 1248
 Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
 405 410 415

gaa tac ttg ttc ttt ccg cat aaa aag aag aaa att gtt cgt act gaa 1296
 Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu
 420 425 430

gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa 1344
 Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu
 435 440 445

ctt gca ctc aag caa caa caa gca cta cag caa cag cag caa caa cca 1392
 Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Gln Pro
 450 455 460

cca caa cca cca caa caa gca cca tca aaa caa gat ggt aca tca acg 1440
 Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
 465 470 475 480

agc cag cct tat gtc aaa ctc cca ccc gca aaa gtt cca gat atg gat 1488
 Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
 485 490 495

ctt gtt aca gtt tcg ttg gta tta aag gaa aag aac gaa acc atc aaa 1536
 Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
 500 505 510

cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gac aag gga 1584
 Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
 515 520 525

ttt atc aat ttg aca gac gat ccg tat cag cca ttt ttc gat att tca 1632
 Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
 530 535 540

acc aat agg gcc gaa gag ttg agc cat att ccg tat tcg tcg att gcg 1680
 Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
 545 550 555 560

gcc aca cac tat cac caa ttc aac aca tcg aac tac atg aac gac caa 1728
 Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
 565 570 575

ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg 1776
 Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
 580 585 590

ttt ttg ggt tct aac ggg gag ttg gta cca tcg aag gca ttt cca cat 1824
 Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
 595 600 605

ttg ctg tct ttg ctt gag gaa aag tat aag gcg aca agt ggg tat att	1872
Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile	
610 615 620	
 gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc	1920
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr	
625 630 635 640	
 aat ggc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg	1968
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met	
645 650 655	
 gcg ttt ccc cag aga ata cgt cga aga gtg ggc agg gct ggc agg gtt	2016
Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val	
660 665 670	
 ttt ttg gac cac cag caa gag tac ccg caa ccg aat ttt cag caa gac	2064
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp	
675 680 685	
 aca gat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc	2112
Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala	
690 695 700	
 att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca	2160
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr	
705 710 715 720	
 act gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca	2208
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro	
725 730 735	
 tct acg caa tct att aga ttt ggg tct atg ttg ttg aat aga aca cgt	2256
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg	
740 745 750	
 aaa tag	2262
Lys	

<210> 10

<211> 754

<212>

<213> Candida albicans

<400> 10

Met Ala Ala Ala Pro Pro Pro Pro Ala Lys Asn Gln Gly Lys Ala Lys

1 5 10 15

Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys

20 25 30

Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser

35 40 45

Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser

50 55 60

Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly

65 70 75 80

Val Asp Lys Asn Glu Glu Glu Glu Val His Leu Gln Gln Val Ile Asn

85 90 95

Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser

100 105 110

Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala

115 120 125

His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile

130 135 140

Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met

145 150 155 160

Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr
 165 170 175

Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu
 180 185 190

Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala
 195 200 205

Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu
 210 215 220

Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr
 225 230 235 240

Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser
 245 250 255

Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro
 260 265 270

Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg
 275 280 285

Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His
 290 295 300

Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr
 305 310 315 320

Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp
 325 330 335

Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr
 340 345 350

Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Ser Met Gln Lys
 355 360 365

Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu
 370 375 380

Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala
 385 390 395 400

Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp
 405 410 415

Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu
 420 425 430

Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu
 435 440 445

Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro
 450 455 460

Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr
 465 470 475 480

Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp
 485 490 495

Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys
 500 505 510

Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly
 515 520 525

Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser
 530 535 540

Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala
 545 550 555 560

Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln
 565 570 575

Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr
 580 585 590

Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His
 595 600 605

Leu Ser Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile
 610 615 620

Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr
 625 630 635 640

Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met
 645 650 655

Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val
 660 665 670

Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp
 675 680 685

Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
 690 695 700

Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
 705 710 715 720

Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
 725 730 735

Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg
 740 745 750

Lys

<210> 11

<211> 447

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1) .. (447)

<400> 11

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Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Glu Gln	
1 5 10 15	
tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa	96
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln	
20 25 30	
tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt	144
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe	
35 40 45	
tta atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat	192
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His	
50 55 60	
ata gat caa tat aat aac tct tct tca ctt cgg aat cat ttg aat aat	240
Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn	
65 70 75 80	
ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa	288
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu	
85 90 95	
gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga	336
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg	
100 105 110	

gtg ata gct agt ata act aaa gaa act tgg aaa att gat tca ttg gat 384
 Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125

aat ttg gtg aaa gaa gta ggt gga act tta caa gtt agt gaa aac ccc 432
 Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
 130 135 140

gat gat atg tgg tga 447
 Asp Asp Met Trp
 145

<210> 12

<211> 149

<212>

<213> Candida albicans

<400> 12

Met Ser Asp Ile Asp Ile Asp Asn Val Leu Asn Leu Glu Glu Glu Gln
 1 5 10 15

Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln
 20 25 30

Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe
 35 40 45

Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His
 50 55 60

Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn
 65 70 75 80

Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu
 85 90 95

Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
 100 105 110

Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125

Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
 130 135 140

Asp Asp Met Trp
 145

<210> 13

<211> 966

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(966)

<400> 13

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 Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
 1 5 10 15

agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa caa 96
 Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
 20 25 30

caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat 144
 Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
 35 40 45

ttt gat ttt ttt gat tta aat cct caa att gat ttc cat gct act aag 192
 Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
 50 55 60

aat ttt tta aga caa tta ttt ggt gat gat aat gga gaa ttt aat tta 240
 Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
 65 70 75 80

agt gaa ata gcc gat tta att tta cga gaa aat tcc gtg ggg aca tca 288
 Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
 85 90 95

att aaa act gaa gga atg gaa agt gat cca ttt gca att tta agt gta 336
 Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
 100 105 110

att aat tta act aat aat tta aat gtg gcc gtg att aaa caa ttg att 384
 Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
 115 120 125

gaa tat att tca aat aaa acc aaa tct aaa act gaa ttc aat att att 432
 Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
 130 135 140

ttg aaa aaa ttg tta acc aat cag aac gat act act aga gat agg aaa 480
 Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
 145 150 155 160

ttt aaa act gga tta ata att agt gaa aga ttt ata aat atg cca gtt 528
 Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
 165 170 175

gaa gtg att cca cca atg tat aaa atg ctt tta caa gaa atg gaa aaa 576
 Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
 180 185 190

gct gaa gat gct cat gaa aat tat gaa ttt gat tat ttt tta att ata 624
 Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
 195 200 205

tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat 672
 Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
 210 215 220

cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag 720
 His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys
 225 230 235 240

aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat 768
 Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
 245 250 255

ctt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt 816
 Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
 260 265 270

gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt 864
 Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
 275 280 285

act gaa tat ggt att gat cct aaa tta agt tta atc tta att gat aaa 912
 Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
 290 295 300

gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct 960
 Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
 305 310 315 320

cca taa 966
 Pro

<210> 14

<211> 322

<212>

<213> Candida albicans

<400> 14

Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val

1 5 10 15

Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln

20 25 30

Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp

35 40 45

Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys

50 55 60

Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu

65 70 75 80

Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser

85 90 95

Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val

100 105 110

Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile

115 120 125

Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile

130 135 140

Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys

145 150 155 160

Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val

165 170 175

Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys

180 185 190

Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
 195 200 205

Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
 210 215 220

His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys
 225 230 235 240

Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
 245 250 255

Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe
 260 265 270

Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe
 275 280 285

Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys
 290 295 300

Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
 305 310 315 320

Pro

<210> 15

<211> 320

<212> DNA

<213> Candida albicans

<400> 15

caattttatctt atgggtccgtt ctggaaattg attttttggtt aaactgctaa tgaattagaa 60

aaatcgcaag atttgcccaa tgaatatatg attgtggaga atgtgccatt attaaataga 120

tttattagta tacctaagga gtatggcgac ttaaattggt cagcatttgt tgcgggtata 180
 attgagggag caattgataa tagtggatto aatgcgatg ttacagcaca caaggtoget 240
 acagatgcaa atccattaag aacagtatct ttgatcaagt ttgacgatto tgtcttaatt 300
 agagagagtt tgagatttgg 320

<210> 16

<211> 295

<212> DNA

<213> Candida albicans

<400> 16

gttcatgttt ggtgactcag agcgtctcaa ctatatttgt cgattataca tacgaactcg 60
 attgagtaag ttgaataaat ttactatctt ttacatcaat gaaagcagtc aaaatgataa 120
 tttattgtcc aaagaggaaa gagattatat acacaaatat ttccagattt tgactcaatt 180
 atataacaac tgtttctctca aaaaactacc acaaattgtg acctatttgg atgacaccag 240
 tgggtggacaa tcaatgatcg ttgagccaga tttagaccag cctgtgttta tcaaaa 295

<210> 17

<211> 392

<212> DNA

<213> Candida albicans

<400> 17

atctctgata tgagatttgg ctttaaaggc gatttaattg aattggctcc agtgggagat 60
 gcacccaaaag atagtccatc cgacatacgt actcatatgg gactccatca tcattcggag 120
 accccacata tggcaggtta tacattgggt gatttggccc atttagccag atcgacttta 180

gctggacaaa gatgcttgag cattcaaaca ttagggagaa tttccataa attgggatta 240
 cataaataca gtatactacc aaaccagctc aatgatcaga gttttacaga tgaatcaaaa 300
 ctatcacttg actttgaaga tagatgtggg acttgataga ccaattacga atcattgaaa 360
 caataacaga ggcagctgat ggaaaaaaga cc 392

<210> 18

<211> 335

<212> DNA

<213> Candida albicans

<400> 18

attccacac cggacgcttc gaggatatgg cccgaggcac acaagtatta caaggatcaa 60
 aagttcaagc agccagagac atatatcaag tttagtgcga cagtagagga cacagtgggt 120
 gtggagtaca atatggacga ggtagatgaa aagttttata gagagacact atgcaagtac 180
 tatcccaaaa agaaaaacaa gtcagatgag aacaatcgaa agtgtactga attggagtgt 240
 gaaacaatct gtgacaagtt ggaaaagacc attgaagcac gacaaccgtt tttgtctatg 300
 gacccagca acattctatc gtacgaggag ttgtc 335

<210> 19

<211> 326

<212> DNA

<213> Candida albicans

<400> 19

agatatagat aatgtattaa atttagaaga agatcaatat gaattaggat ttaaagaagg 60
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atttcaacga tttttaatca ttggttatat tcaagaatta atgaaatttt ggttatocca 180
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